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RESULT 1
US-09-908-975-10633
Sequence 10633, Application US/09/908,975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINZ, Eli
; APPLICANT: MINTZ, Liat
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICING
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 10633
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-908-975-10633

Query Match 1.2%; Score 60; DB 1; Length 60;
 Best Local Similarity 100.0%; Pred. No. 0.37; 0; Mismatches 0; Indels 0; Gaps 0;

Matches 60; Conservative 0; General Information: Keen, Randy
 APPLICANT: Koder, Alan
 APPLICANT: Evans, David
 TITLE OF INVENTION: Apparatus For the Automated Synthesis of Polynucleotides
 TITLE OF INVENTION: Polynucleotides
 FILE REFERENCE: 66663-031(EA5438)
 CURRENT APPLICATION NUMBER: US/10/431,627
 CURRENT FILING DATE: 2003-05-06

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416	20	0.4	20	1	US-10-601-140A-1	Sequence 1, App	c 489	18.8	0.4	25	1	US-10-719-956-643654
417	20	0.4	20	1	US-10-601-140A-2	Sequence 2, App	c 490	18.4	0.4	20	1	US-10-831-901A-29730
418	20	0.4	20	1	US-10-601-140A-3	Sequence 3, App	c 491	18.4	0.4	24	1	US-10-374-366-201
419	20	0.4	20	1	US-10-601-140A-4	Sequence 4, App	c 492	18	0.4	18	1	US-10-849-072-21
420	20	0.4	20	1	US-10-601-140A-6	Sequence 5, App	c 493	18	0.4	18	1	US-10-719-956-44393
421	20	0.4	20	1	US-10-601-140A-7	Sequence 6, App	c 494	18	0.4	18	1	US-10-831-778-913
422	20	0.4	20	1	US-10-601-140A-8	Sequence 7, App	c 495	18	0.4	18	1	US-10-831-778-919
423	20	0.4	20	1	US-10-601-140A-9	Sequence 8, App	c 496	18	0.4	18	1	US-10-831-901A-29731
424	20	0.4	20	1	US-10-601-140A-10	Sequence 9, App	c 497	18	0.4	18	1	US-10-674-159A-112
425	20	0.4	20	1	US-10-601-140A-12	Sequence 10, App	c 498	18	0.4	18	1	US-10-776-917-141
426	20	0.4	20	1	US-10-601-140A-34	Sequence 11, App	c 499	18	0.4	18	1	US-10-766-906-9
427	20	0.4	20	1	US-10-601-140A-40	Sequence 12, App	c 500	18	0.4	18	1	US-10-638-141-90
428	20	0.4	20	1	US-10-601-140A-44	Sequence 13, App	c 501	18	0.4	18	1	US-10-776-934-741
429	20	0.4	20	1	US-10-787-831-22	Sequence 14, App	c 502	18	0.4	18	1	US-10-776-933-150
430	20	0.4	20	1	US-10-831-901A-29732	Sequence 15, App	c 503	18	0.4	18	1	US-10-884-617-2
431	20	0.4	20	1	US-10-831-901A-29733	Sequence 16, App	c 504	18	0.4	18	1	US-10-669-962-27
432	20	0.4	20	1	US-10-831-901A-29734	Sequence 17, App	c 505	18	0.4	18	1	US-10-503-120-1
433	20	0.4	20	1	US-10-831-901A-29735	Sequence 18, App	c 506	18	0.4	18	1	US-10-503-120-8
434	20	0.4	20	1	US-10-831-901A-29736	Sequence 19, App	c 507	18	0.4	18	1	US-10-503-120-9
435	20	0.4	20	1	US-10-787-831-22	Sequence 20, App	c 508	18	0.4	18	1	US-10-503-120-10
436	20	0.4	20	1	US-10-789-831-23	Sequence 21, App	c 509	18	0.4	18	1	US-10-884-617-2
437	20	0.4	20	1	US-10-789-831-24	Sequence 22, App	c 510	18	0.4	18	1	US-10-775-973-10
438	20	0.4	20	1	US-10-661-402-12	Sequence 23, App	c 511	18	0.4	18	1	US-11-024-428-7
439	20	0.4	20	1	US-10-661-402-15	Sequence 24, App	c 512	18	0.4	19	1	US-10-913-246-22
440	20	0.4	20	1	US-10-847-502-10	Sequence 25, App	c 513	18	0.4	19	1	US-10-934-890-22
441	20	0.4	20	1	US-10-847-502-15	Sequence 26, App	c 514	18	0.4	20	1	US-10-503-120-21
442	20	0.4	20	1	US-10-925-154-35	Sequence 27, App	c 515	18	0.4	18	1	US-10-786-720-113
443	20	0.4	20	1	US-10-912-246-23	Sequence 28, App	c 516	17.8	0.4	21	1	US-10-712-295-850
444	20	0.4	20	1	US-10-934-890-23	Sequence 29, App	c 517	17.4	0.3	20	1	US-10-920-612-20
445	20	0.4	20	1	US-10-995-995-6	Sequence 30, App	c 518	17.4	0.3	20	1	US-10-931-901A-29729
446	20	0.4	20	1	US-10-314-578-60	Sequence 31, App	c 519	17.4	0.3	20	1	US-10-374-686-4
447	19.8	0.4	24	1	US-10-681-773-75257	Sequence 32, App	c 520	17.4	0.3	21	1	US-10-412-137-34
448	19.2	0.4	24	1	US-09-756-479-60	Sequence 33, App	c 521	17.4	0.3	22	1	US-10-723-947-34
449	19.2	0.4	24	1	US-09-776-479-60	Sequence 34, App	c 522	17.4	0.3	22	1	US-09-263-959-808
450	19.2	0.4	24	1	US-10-112-653-54	Sequence 35, App	c 523	17.2	0.3	22	1	US-10-361-002-33
451	19.2	0.4	24	1	US-10-917-995-60	Sequence 36, App	c 524	17.2	0.3	22	1	US-10-361-004-33
452	19.2	0.4	24	1	US-10-719-900-228030	Sequence 37, App	c 525	17.2	0.3	22	1	US-08-085-579-5
453	19.2	0.4	24	1	US-10-719-900-286591	Sequence 38, App	c 526	17	0.3	17	1	US-10-467-731-5
454	19.2	0.4	25	1	US-10-098-263B-76253	Sequence 39, App	c 527	17	0.3	17	1	US-10-952-768-6
455	19.2	0.4	25	1	US-10-719-900-18911	Sequence 40, App	c 528	17	0.3	17	1	US-09-944-851-6
456	19.2	0.4	25	1	US-10-719-900-228029	Sequence 41, App	c 529	17	0.3	17	1	US-10-871-222-300
457	19.2	0.4	25	1	US-10-719-900-956708	Sequence 42, App	c 530	17	0.3	17	1	US-10-871-949-749-5
458	19.2	0.4	25	1	US-10-719-956-68653	Sequence 43, App	c 531	17	0.3	17	1	US-10-337-060-6
459	19.2	0.4	25	1	US-10-719-956-369528	Sequence 44, App	c 532	17	0.3	17	1	US-10-668-955-6
460	19.2	0.4	25	1	US-10-719-956-467347	Sequence 45, App	c 533	17	0.3	17	1	US-10-669-962-28
461	19.2	0.4	25	1	US-10-098-263B-76254	Sequence 46, App	c 534	17	0.3	18	1	US-10-665-962-29
462	19.2	0.4	25	1	US-10-719-900-872675	Sequence 47, App	c 535	17	0.3	19	1	US-10-871-222-300
463	19.2	0.4	25	1	US-10-719-900-940-1	Sequence 48, App	c 536	17	0.3	19	1	US-10-871-222-300
464	19.2	0.4	25	1	US-10-719-900-956708	Sequence 49, App	c 537	17	0.3	20	1	US-08-809-223A-23
465	19.2	0.4	25	1	US-10-719-956-369528	Sequence 50, App	c 538	17	0.3	20	1	US-10-271-344-23
466	19.2	0.4	25	1	US-10-719-956-520734	Sequence 51, App	c 539	17	0.3	22	1	US-10-397-131-7
467	19.2	0.4	25	1	US-10-719-956-520734	Sequence 52, App	c 540	17	0.3	22	1	US-10-160-786-72
468	19.2	0.4	25	1	US-10-760-940-1	Sequence 53, App	c 541	16.8	0.3	20	1	US-10-667-022-72
469	19.2	0.4	25	1	US-10-913-246-24	Sequence 54, App	c 542	16.8	0.3	20	1	US-10-809-189-2442
470	19.2	0.4	25	1	US-10-934-890-24	Sequence 55, App	c 543	16.8	0.3	20	1	US-10-831-001A-29728
471	19.2	0.4	25	1	US-10-700-884-23	Sequence 56, App	c 544	16.8	0.3	21	1	US-10-274-095-21

c 107	24	0.5	28	1 US-10-942-251-2	Sequence 12, App1	c 180	20	0.4	20	1 US-10-160-786-55
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c 110	23	0.5	23	1 US-10-160-786-5	Sequence 5, App1	c 182	20	0.4	20	1 US-10-160-786-57
c 111	23	0.5	23	1 US-10-160-786-5	Sequence 6, App1	c 183	20	0.4	20	1 US-10-160-786-58
c 112	23	0.5	23	1 US-10-667-022-6	Sequence 5, App1	c 184	20	0.4	20	1 US-10-160-786-59
c 113	23	0.5	23	1 US-10-048-866D-10	Sequence 10, App1	c 185	20	0.4	20	1 US-10-160-786-60
c 114	22	0.4	24	1 US-10-721-793-285	Sequence 285, App	c 186	20	0.4	20	1 US-10-160-786-62
c 115	21.8	0.4	25	1 US-10-719-956-45762	Sequence 45762, A	c 187	20	0.4	20	1 US-10-160-786-63
c 116	21.8	0.4	25	1 US-10-719-956-150046	Sequence 150046,	c 188	20	0.4	20	1 US-10-160-786-64
c 117	21.8	0.4	25	1 US-10-719-956-159330	Sequence 159330,	c 189	20	0.4	20	1 US-10-160-786-65
c 118	21.8	0.4	25	1 US-10-719-956-529364	Sequence 529364,	c 190	20	0.4	20	1 US-10-160-786-66
c 119	21.2	0.4	27	1 US-10-085-906-78	Sequence 78, App1	c 191	20	0.4	20	1 US-10-160-786-67
c 120	21	0.4	21	1 US-08-085-813-4	Sequence 4, App1	c 192	20	0.4	20	1 US-10-160-786-68
c 121	21	0.4	21	1 US-10-831-778-912	Sequence 912, App1	c 193	20	0.4	20	1 US-10-160-786-69
c 122	21	0.4	21	1 US-10-830-287A-7	Sequence 7, App1	c 194	20	0.4	20	1 US-10-160-786-70
c 123	21	0.4	21	1 US-10-601-140A-43	Sequence 43, App1	c 195	20	0.4	20	1 US-10-160-786-71
c 124	20.4	0.4	22	1 US-10-601-140A-45	Sequence 45, App1	c 196	20	0.4	20	1 US-10-160-786-72
c 125	20.4	0.4	25	1 US-10-930-301-44	Sequence 44, App1	c 197	20	0.4	20	1 US-10-160-786-73
c 126	20.4	0.4	26	1 US-10-930-301-98	Sequence 98, App1	c 198	20	0.4	20	1 US-10-160-786-74
c 127	20.4	0.4	25	1 US-10-664-000-3	Sequence 3, App1	c 199	20	0.4	20	1 US-10-160-786-75
c 128	20.2	0.4	22	1 US-10-601-140A-32	Sequence 32, App1	c 200	20	0.4	20	1 US-10-160-786-76
c 129	20.2	0.4	22	1 US-10-719-956-43761	Sequence 45761, A	c 201	20	0.4	20	1 US-10-160-786-77
c 130	20.2	0.4	25	1 US-10-719-956-150045	Sequence 150045,	c 202	20	0.4	20	1 US-10-160-786-78
c 131	20.2	0.4	25	1 US-10-719-956-159329	Sequence 159329,	c 203	20	0.4	20	1 US-10-160-786-79
c 132	20.2	0.4	25	1 US-10-719-956-415763	Sequence 415763,	c 204	20	0.4	20	1 US-10-160-786-80
c 133	20.2	0.4	25	1 US-10-719-956-415763	Sequence 144, App	c 205	20	0.4	20	1 US-10-160-786-81
c 134	20.2	0.4	26	1 US-10-085-906-144	Sequence 55, App1	c 206	20	0.4	20	1 US-10-160-786-82
c 135	20	0.4	20	1 US-09-976-900A-55	Sequence 11, App1	c 207	20	0.4	20	1 US-10-160-786-83
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c 138	20	0.4	20	1 US-10-160-786-13	Sequence 14, App1	c 210	20	0.4	20	1 US-10-160-786-86
c 139	20	0.4	20	1 US-10-160-786-14	Sequence 15, App1	c 211	20	0.4	20	1 US-10-160-786-87
c 140	20	0.4	20	1 US-10-160-786-15	Sequence 16, App1	c 212	20	0.4	20	1 US-10-160-786-88
c 141	20	0.4	20	1 US-10-160-786-16	Sequence 17, App1	c 213	20	0.4	20	1 US-10-160-786-89
c 142	20	0.4	20	1 US-10-160-786-17	Sequence 18, App1	c 214	20	0.4	20	1 US-10-160-786-90
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c 145	20	0.4	20	1 US-10-160-786-20	Sequence 21, App1	c 217	20	0.4	20	1 US-10-160-786-93
c 146	20	0.4	20	1 US-10-160-786-21	Sequence 22, App1	c 218	20	0.4	20	1 US-10-160-786-94
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c 150	20	0.4	20	1 US-10-160-786-25	Sequence 26, App1	c 222	20	0.4	20	1 US-10-160-786-98
c 151	20	0.4	20	1 US-10-160-786-26	Sequence 27, App1	c 223	20	0.4	20	1 US-10-160-786-99
c 152	20	0.4	20	1 US-10-160-786-27	Sequence 28, App1	c 224	20	0.4	20	1 US-10-160-786-100
c 153	20	0.4	20	1 US-10-160-786-28	Sequence 29, App1	c 225	20	0.4	20	1 US-10-160-786-101
c 154	20	0.4	20	1 US-10-160-786-29	Sequence 30, App1	c 226	20	0.4	20	1 US-10-160-786-102
c 155	20	0.4	20	1 US-10-160-786-30	Sequence 31, App1	c 227	20	0.4	20	1 US-10-160-786-103
c 156	20	0.4	20	1 US-10-160-786-31	Sequence 32, App1	c 228	20	0.4	20	1 US-10-160-786-104
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c 158	20	0.4	20	1 US-10-160-786-33	Sequence 34, App1	c 230	20	0.4	20	1 US-10-160-786-106
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c 160	20	0.4	20	1 US-10-160-786-35	Sequence 36, App1	c 232	20	0.4	20	1 US-10-160-786-108
c 161	20	0.4	20	1 US-10-160-786-36	Sequence 37, App1	c 233	20	0.4	20	1 US-10-160-786-109
c 162	20	0.4	20	1 US-10-160-786-37	Sequence 38, App1	c 234	20	0.4	20	1 US-10-160-786-110
c 163	20	0.4	20	1 US-10-160-786-38	Sequence 39, App1	c 235	20	0.4	20	1 US-10-160-786-111
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c 165	20	0.4	20	1 US-10-160-786-40	Sequence 41, App1	c 237	20	0.4	20	1 US-10-160-786-113
c 166	20	0.4	20	1 US-10-160-786-41	Sequence 42, App1	c 238	20	0.4	20	1 US-10-160-786-114
c 167	20	0.4	20	1 US-10-160-786-42	Sequence 43, App1	c 239	20	0.4	20	1 US-10-160-786-115
c 168	20	0.4	20	1 US-10-160-786-43	Sequence 44, App1	c 240	20	0.4	20	1 US-10-160-786-116
c 169	20	0.4	20	1 US-10-160-786-44	Sequence 45, App1	c 241	20	0.4	20	1 US-10-160-786-117
c 170	20	0.4	20	1 US-10-160-786-45	Sequence 46, App1	c 242	20	0.4	20	1 US-10-160-786-118
c 171	20	0.4	20	1 US-10-160-786-46	Sequence 47, App1	c 243	20	0.4	20	1 US-10-160-786-119
c 172	20	0.4	20	1 US-10-160-786-47	Sequence 48, App1	c 244	20	0.4	20	1 US-10-160-786-120
c 173	20	0.4	20	1 US-10-160-786-48	Sequence 49, App1	c 245	20	0.4	20	1 US-10-160-786-121
c 174	20	0.4	20	1 US-10-160-786-49	Sequence 50, App1	c 246	20	0.4	20	1 US-10-160-786-122
c 175	20	0.4	20	1 US-10-160-786-50	Sequence 51, App1	c 247	20	0.4	20	1 US-10-160-786-123
c 176	20	0.4	20	1 US-10-160-786-51	Sequence 52, App1	c 248	20	0.4	20	1 US-10-160-786-124
c 177	20	0.4	20	1 US-10-160-786-52	Sequence 53, App1	c 249	20	0.4	20	1 US-10-160-786-125
c 178	20	0.4	20	1 US-10-160-786-53	Sequence 54, App1	c 250	20	0.4	20	1 US-10-160-786-126
c 179	20	0.4	20	1 US-10-160-786-54	Sequence 55, App1	c 251	20	0.4	20	1 US-10-160-786-127

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OM nucleic - nucleic search, using SW model
Run on: August 18, 2005, 08:50:58 ; Search time 45 Seconds
(without alignments)
.3.758 Million cell updates/sec

Title: US-10-667-022-4
Perfect score: 5085
Sequence: 1 ggatccccgggtgcaga.....tcgagggggccggtaac 5085

Scoring table: IDENTITY_NUC
Gapop 10⁻⁰, Gapext 0.5

Searched: 776 seqs, 16629 residues

Total number of hits satisfying chosen parameters: 1552

Minimum DB seq length: 8
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 782 summaries

Database : fetcharmp.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1552

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	60	1.2	60	1	US-09-908-975-10633	Sequence 10633, A
2	40.6	0.8	50	1	US-10-431-621-3	Sequence 3, Appli
3	40.6	0.8	50	1	US-10-450-761-6	Sequence 6, Appli
4	40	0.8	40	1	US-10-661-415-20	Sequence 20, Appli
5	40	0.8	40	1	US-10-661-415-23	Sequence 23, Appli
6	40	0.8	40	1	US-10-463-574A-1	Sequence 1, Appli
7	40	0.8	40	1	US-10-463-574A-2	Sequence 2, Appli
8	40	0.8	40	1	US-10-661-402-20	Sequence 20, Appli
9	40	0.8	40	1	US-10-661-402-23	Sequence 23, Appli
10	38.4	0.8	51	1	US-10-489-136-31	Sequence 31, Appli
11	35	0.7	35	1	US-10-601-140A-11	Sequence 11, Appli
12	35	0.7	35	1	US-10-601-140A-12	Sequence 12, Appli
13	31.4	0.6	33	1	US-10-848-922-98	Sequence 98, Appli
14	31.4	0.6	33	1	US-10-880-422A-41	Sequence 41, Appli
15	31.4	0.6	40	1	US-10-450-761-4	Sequence 4, Appli
16	30	0.6	30	1	US-11-021-367-10	Sequence 10, Appli
17	28	0.6	29	1	US-10-764-799-8	Sequence 8, Appli
18	28	0.6	37	1	US-10-055-908-225	Sequence 225, App
19	27.4	0.5	31	1	US-10-933-118-136	Sequence 136, App
20	27	0.5	27	1	US-10-831-776-911	Sequence 911, App
21	27	0.5	36	1	US-10-055-908-294	Sequence 294, App
22	26.8	0.5	31	1	US-10-849-491-1	Sequence 1, Appli
23	26.8	0.5	32	1	US-10-942-253-29	Sequence 29, Appli
24	26.4	0.5	28	1	US-10-942-251-8	Sequence 7, Appli
25	26	0.5	26	1	US-10-160-765-6	Sequence 136, Appli
26	26	0.5	26	1	US-10-667-022-7	Sequence 911, Appli
27	26	0.5	36	1	US-10-787-442-38	Sequence 38, Appli
28	26	0.5	26	1	US-10-959-164-7	Sequence 7, Appli
29	25.2	0.5	26	1	US-10-963-164-6	Sequence 6, Appli
30	25.2	0.5	27	1	US-09-859-012-37	Sequence 37, Appli
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 ; Patent No. 5648210
 ; GENERAL INFORMATION:
 ; APPLICANT: John W. Pierce

ALIGNMENTS

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Post-processing: Maximum Match 0%

Listing first 241 summaries

Database : fech4rn1.seq*

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C	262	20	0.4	20	1	ADL4674	C	335	18.2	0.4	24	1	AZT07017
C	263	20	0.4	20	1	ADL4669	C	336	18.2	0.4	24	1	ABQ78896
C	264	20	0.4	20	1	ADL4569	C	337	18.2	0.4	24	1	ABT19218
C	265	20	0.4	20	1	ADL4570	C	338	18.2	0.4	24	1	ABZ59876
C	266	20	0.4	20	1	ADL4579	C	339	18.2	0.4	24	1	ADU8152
C	267	20	0.4	20	1	ADL4641	C	340	18	0.4	18	1	ADR32355
C	268	20	0.4	20	1	ADL4673	C	341	18	0.4	18	1	ABD57967
C	269	20	0.4	20	1	ADL4685	C	342	18	0.4	22	1	ADM3751
C	270	20	0.4	20	1	ADL4615	C	343	17.8	0.4	21	1	ADM19213
C	271	20	0.4	20	1	ADL4619	C	344	17.8	0.4	22	1	ADP32218
C	272	20	0.4	20	1	ADL4641	C	345	17.4	0.3	19	1	AKW87932
C	273	20	0.4	20	1	ADL4648	C	346	17.4	0.3	19	1	ADM83687
C	274	20	0.4	20	1	ADL4673	C	347	17.4	0.3	19	1	AMH5849
C	275	20	0.4	20	1	ADL4685	C	348	17.4	0.3	20	1	AMJ14499
C	276	20	0.4	20	1	ADL4567	C	349	17.4	0.3	20	1	ADM1861
C	277	20	0.4	20	1	ADL4574	C	350	17.4	0.3	20	1	ADP32402
C	278	20	0.4	20	1	ADL4584	C	351	17.4	0.3	21	1	ABF87932
C	279	20	0.4	20	1	ADL4632	C	352	17.4	0.3	22	1	ADP42646
C	280	20	0.4	20	1	ADL4672	C	353	17.4	0.3	23	1	AKW9371
C	281	20	0.4	20	1	ADL4679	C	354	17.4	0.3	23	1	ADM45480
C	282	20	0.4	20	1	ADL4688	C	355	17.2	0.3	22	1	ADP32402
C	283	20	0.4	20	1	ADL4696	C	356	17.2	0.3	22	1	ABP32106
C	284	20	0.4	20	1	ADL4701	C	357	17.2	0.3	22	1	ABD32106
C	285	20	0.4	20	1	ADL4572	C	358	17.2	0.3	22	1	ABD67796
C	286	20	0.4	20	1	ADL4575	C	359	17.2	0.3	22	1	ADM6995
C	287	20	0.4	20	1	ADL4604	C	360	17	0.3	17	1	ADM19091
C	288	20	0.4	20	1	ADL4625	C	361	17	0.3	17	1	ADM17930
C	289	20	0.4	20	1	ADL4634	C	362	17	0.3	17	1	ADM16052
C	290	20	0.4	20	1	ADL4653	C	363	17	0.3	17	1	ADM32106
C	291	20	0.4	20	1	ADL4670	C	364	17	0.3	17	1	ADM2194
C	292	20	0.4	20	1	ADL4678	C	365	17	0.3	17	1	ADM5203
C	293	20	0.4	20	1	ADL4698	C	366	17	0.3	19	1	ADM18161
C	294	20	0.4	20	1	ADL4568	C	367	17	0.3	20	1	ADM18426
C	295	20	0.4	20	1	ADL4578	C	368	17	0.3	20	1	ADM20641
C	296	20	0.4	20	1	ADL4580	C	369	17	0.3	22	1	ADM15659
C	297	20	0.4	20	1	ADL4642	C	370	16.8	0.3	20	1	ADM126737
C	298	20	0.4	20	1	ADL4645	C	371	16.8	0.3	20	1	ADM59618
C	299	20	0.4	20	1	ADL4668	C	372	16.8	0.3	20	1	ADM06717
C	300	20	0.4	20	1	ADL4676	C	373	16.8	0.3	20	1	ADM17444
C	301	20	0.4	20	1	ADL4690	C	374	16.8	0.3	20	1	ADM17777
C	302	20	0.4	20	1	ADL4692	C	375	16.8	0.3	20	1	ADM22895
C	303	20	0.4	20	1	ADL4566	C	376	16.8	0.3	20	1	ADM8790
C	304	20	0.4	20	1	ADL4631	C	377	16.8	0.3	20	1	ADM59618
C	305	20	0.4	20	1	ADL4655	C	378	16.8	0.3	20	1	ADM15944
C	306	20	0.4	20	1	ADL4661	C	379	16.8	0.3	20	1	ADM15962
C	307	20	0.4	20	1	ADL4665	C	380	16.8	0.3	21	1	ADM17777
C	308	20	0.4	20	1	ADL4683	C	381	16.8	0.3	21	1	ACCC7852
C	309	20	0.4	20	1	ADR9805	C	382	16.8	0.3	21	1	ADM94102
C	310	20	0.4	21	1	ADX08666	C	383	16.8	0.3	21	1	ADM09421
C	311	20	0.4	21	1	AAV717394	C	384	16.8	0.3	22	1	AVV27859
C	312	20	0.4	24	1	ADK5560	C	385	16.8	0.3	22	1	ADM80013
C	313	20	0.4	24	1	ADK5557	C	386	16.8	0.3	22	1	ADM17777
C	314	19.6	0.4	25	1	AAQ47178	C	387	16.8	0.3	22	1	ADM44228
C	315	19.4	0.4	24	1	ABA01951	C	388	16.8	0.3	22	1	ADM97099
C	316	19.2	0.4	24	1	AAK9935	C	389	16.8	0.3	22	1	ADM59856
C	317	19.2	0.4	24	1	ABS77156	C	390	16.8	0.3	22	1	ADM64016
C	318	19.2	0.4	24	1	ACD93368	C	391	16.8	0.3	22	1	ACP942669
C	319	19.2	0.4	24	1	ABD36437	C	392	16.8	0.3	22	1	ADM04018
C	320	19.2	0.4	24	1	ADG76001	C	393	16.8	0.3	22	1	ADM16768
C	321	19.2	0.4	24	1	ADG76035	C	394	16.4	0.3	18	1	ADM6310
C	322	19.2	0.4	25	1	ACT17623	C	395	16.4	0.3	19	1	ADM33800
C	323	19.2	0.4	25	1	ACT17622	C	396	16.4	0.3	20	1	ADM76854
C	324	19.2	0.4	19	1	ADM52089	C	397	16.4	0.3	20	1	ADM77487
C	325	19	0.4	1	ADR82260	C	398	16.4	0.3	20	1	ADM825728	

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108	20	0.4	20	1	AD126762		181	20	0.4	20	1	AD134660	Phosphoinositide-3
109	20	0.4	20	1	AD126766		182	20	0.4	20	1	AD134677	Phosphoinositide-3
110	20	0.4	20	1	AD126773		183	20	0.4	20	1	AD134700	Phosphoinositide-3
111	20	0.4	20	1	AD126781		184	20	0.4	20	1	AD134602	ISIS antisense oli
112	20	0.4	20	1	AD126796		185	20	0.4	20	1	AD134605	Phosphoinositide-3
113	20	0.4	20	1	AD126800		186	20	0.4	20	1	AD134651	Phosphoinositide-3
114	20	0.4	20	1	AD126679		187	20	0.4	20	1	AD134671	Phosphoinositide-3
115	20	0.4	20	1	AD126696		188	20	0.4	20	1	AD134699	Phosphoinositide-3
116	20	0.4	20	1	AD126697		189	20	0.4	20	1	AD134576	ISIS antisense oli
117	20	0.4	20	1	AD126706		190	20	0.4	20	1	AD134598	Phosphoinositide-3
118	20	0.4	20	1	AD126720		191	20	0.4	20	1	AD134607	ISIS antisense oli
119	20	0.4	20	1	AD126750		192	20	0.4	20	1	AD134614	Phosphoinositide-3
120	20	0.4	20	1	AD126753		193	20	0.4	20	1	AD134616	ISIS antisense oli
121	20	0.4	20	1	AD126788		194	20	0.4	20	1	AD134630	ISIS antisense oli
122	20	0.4	20	1	AD126789		195	20	0.4	20	1	AD134640	ISIS antisense oli
123	20	0.4	20	1	AD126802		196	20	0.4	20	1	AD134649	Phosphoinositide-3
124	20	0.4	20	1	AD126689		197	20	0.4	20	1	AD134679	Phosphoinositide-3
125	20	0.4	20	1	AD126721		198	20	0.4	20	1	AD134687	Phosphoinositide-3
126	20	0.4	20	1	AD126736		199	20	0.4	20	1	AD134671	ISIS antisense oli
127	20	0.4	20	1	AD126785		200	20	0.4	20	1	AD134571	ISIS antisense oli
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129	20	0.4	20	1	AD126774		202	20	0.4	20	1	AD134613	ISIS antisense oli
130	20	0.4	20	1	AD126778		203	20	0.4	20	1	AD134621	Phosphoinositide-3
131	20	0.4	20	1	AD126782		204	20	0.4	20	1	AD134652	Phosphoinositide-3
132	20	0.4	20	1	AD126785		205	20	0.4	20	1	AD134664	Phosphoinositide-3
133	20	0.4	20	1	AD126799		206	20	0.4	20	1	AD134682	Phosphoinositide-3
134	20	0.4	20	1	AD126801		207	20	0.4	20	1	AD134684	Phosphoinositide-3
135	20	0.4	20	1	AD126803		208	20	0.4	20	1	AD134608	ISIS antisense oli
136	20	0.4	20	1	AD126686		209	20	0.4	20	1	AD134618	Phosphoinositide-3
137	20	0.4	20	1	AD126687		210	20	0.4	20	1	AD134633	Phosphoinositide-3
138	20	0.4	20	1	AD126699		211	20	0.4	20	1	AD134682	Phosphoinositide-3
139	20	0.4	20	1	AD126700		212	20	0.4	20	1	AD134647	ISIS antisense oli
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141	20	0.4	20	1	AD126711		214	20	0.4	20	1	AD134583	ISIS antisense oli
142	20	0.4	20	1	AD126763		215	20	0.4	20	1	AD134592	ISIS antisense oli
143	20	0.4	20	1	AD126783		216	20	0.4	20	1	AD134595	ISIS antisense oli
144	20	0.4	20	1	AD126786		217	20	0.4	20	1	AD134606	ISIS antisense oli
145	20	0.4	20	1	AD126792		218	20	0.4	20	1	AD134617	Phosphoinositide-3
146	20	0.4	20	1	AD126810		219	20	0.4	20	1	AD134620	Phosphoinositide-3
147	20	0.4	20	1	AD126812		220	20	0.4	20	1	AD134623	ISIS antisense oli
148	20	0.4	20	1	AD126677		221	20	0.4	20	1	AD134629	Phosphoinositide-3
149	20	0.4	20	1	AD126694		222	20	0.4	20	1	AD134663	Phosphoinositide-3
150	20	0.4	20	1	AD126712		223	20	0.4	20	1	AD134666	Phosphoinositide-3
151	20	0.4	20	1	AD126714		224	20	0.4	20	1	AD134617	ISIS antisense oli
152	20	0.4	20	1	AD126718		225	20	0.4	20	1	AD134681	Phosphoinositide-3
153	20	0.4	20	1	AD126722		226	20	0.4	20	1	AD134686	Phosphoinositide-3
154	20	0.4	20	1	AD126723		227	20	0.4	20	1	AD134694	Phosphoinositide-3
155	20	0.4	20	1	AD126777		228	20	0.4	20	1	AD134586	Phosphoinositide-3
156	20	0.4	20	1	AD126792		229	20	0.4	20	1	AD134588	Phosphoinositide-3
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158	20	0.4	20	1	AD126725		231	20	0.4	20	1	AD134591	Phosphoinositide-3
159	20	0.4	20	1	AD126731		232	20	0.4	20	1	AD134593	Phosphoinositide-3
160	20	0.4	20	1	AD126740		233	20	0.4	20	1	AD134689	Phosphoinositide-3
161	20	0.4	20	1	AD126746		234	20	0.4	20	1	AD134593	Phosphoinositide-3
162	20	0.4	20	1	AD126755		235	20	0.4	20	1	AD134594	Phosphoinositide-3
163	20	0.4	20	1	AD126772		236	20	0.4	20	1	AD134596	Phosphoinositide-3
164	20	0.4	20	1	AD126776		237	20	0.4	20	1	AD134601	Phosphoinositide-3
165	20	0.4	20	1	AD126680		238	20	0.4	20	1	AD134606	Phosphoinositide-3
166	20	0.4	20	1	AD126685		239	20	0.4	20	1	AD134611	Phosphoinositide-3
167	20	0.4	20	1	AD126698		240	20	0.4	20	1	AD134622	Phosphoinositide-3
168	20	0.4	20	1	AD126728		241	20	0.4	20	1	AD134633	Phosphoinositide-3
169	20	0.4	20	1	AD126738		242	20	0.4	20	1	AD134662	Phosphoinositide-3
170	20	0.4	20	1	AD126787		243	20	0.4	20	1	AD134680	Phosphoinositide-3
171	20	0.4	20	1	AD126809		244	20	0.4	20	1	AD134691	Phosphoinositide-3
172	20	0.4	20	1	AD134585		245	20	0.4	20	1	AD134588	Phosphoinositide-3
173	20	0.4	20	1	AD134599		246	20	0.4	20	1	AD134643	Phosphoinositide-3
174	20	0.4	20	1	AD134603		247	20	0.4	20	1	AD134643	Phosphoinositide-3
175	20	0.4	20	1	AD134610		248	20	0.4	20	1	AD134646	Phosphoinositide-3
176	20	0.4	20	1	AD134637		249	20	0.4	20	1	AD134695	Phosphoinositide-3
177	20	0.4	20	1	AD134638		250	20	0.4	20	1	AD134697	Phosphoinositide-3
178	20	0.4	20	1	AD134654		251	20	0.4	20	1	AD134590	Phosphoinositide-3
179	20	0.4	20	1	AD134656		252	20	0.4	20	1	AD134627	Phosphoinositide-3

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Om nucleic - nucleic search, using sw model

Run on: August 18, 2005, 08:36:54 ; Search time 32 Seconds

(without alignments)

3.559 Million cell updates/sec

Title: US-10-667-022-4

Perfect score: 5085

Sequence: 1 ggatcccccgggtcgagga.....tcggggggccggtaacc 5085

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched:

536 seqs, 11197 residues

Total number of hits satisfying chosen parameters: 1072

Minimum DB seq length: 8

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 542 summaries

Database : fetch4mg seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	60	1.2	60 1 ABM37885	Human spliced tran
2	44	0.9	54 1 ACTN4858	Cotton androecium
3	41.2	0.8	51 1 ACN51213	Cotton androecium
4	41.2	0.8	51 1 ACNS1219	T50 element used 1
5	40.6	0.8	50 1 AD574280	A50 element used 1
6	40.6	0.8	50 1 AD574279	Oligonucleotide oc
7	37.8	0.7	50 1 ADR18577	238PIB2 gene relat
8	33.8	0.7	43 1 ADI197735	Sequence of the 5'
9	33.2	0.7	40 1 AAC06506	Antitumoural phosp
10	27.7	0.5	35 1 AAT33815	Antitumoural phosp
11	27	0.5	35 1 AAT33823	Antitumoural phosp
12	27	0.5	25 1 ADH26672	Human PI3K regulat
13	26	0.5	26 1 ADL4561	Human phosphoinosi
14	26	0.5	34 1 AAC0605	Tomato spotted wit
15	25.4	0.5	27 1 ADP51048	Duo binding molety
16	25	0.5	27 1 ADR42246	Microarray synthe
17	24	0.5	24 1 ADR42249	Microarray synthe
18	24	0.5	30 1 AAT03154	Levensnase mutan
19	24	0.5	21 1 AAV06992	Human PI3K regulat
20	23	0.5	23 1 ADH26671	Human PI3K regulat
21	23	0.5	23 1 ADH26670	Human PI3K regulat
22	23	0.5	23 1 ADL4560	Human phosphoinosi
23	23	0.5	23 1 ADL4559	Human phosphoinosi
24	22	0.4	25 1 ADR42220	Caenorhabditis ele
25	21	0.4	21 1 AAV03154	PCR primer BKSB E
26	21	0.4	24 1 AAV06992	Inverse PCR Primer
27	21	0.4	24 1 ABA0435	Human GM2 activati
28	21	0.4	24 1 ABA05961	Human molecular ch
29	21	0.4	24 1 ABZ57354	Human zinc finger
30	21	0.4	24 1 ADR42221	Caenorhabditis ele
31	20.4	0.4	24 1 ABA059469	Human natural resu
32	20.2	0.4	22 1 ADI13095	Oligo dT PCR prime
33	20	0.4	1 AAF76082	pBluecript vector
34	20	0.4	1 AAEF76459	Maize ZmMADS2 codi
35	20	0.4	1 ADH26756	Human PI3K regulat
36	20	0.4	1 ADH26709	Human PI3K regulat
37	20	0.4	1 ADH26726	Human PI3K regulat
38	20	0.4	1 ADH26733	Human PI3K regulat
39	20	0.4	1 ADH26739	Human PI3K regulat
40	20	0.4	1 ADH26749	Human PI3K regulat
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43	20	0.4	1 ADH26681	Human PI3K regulat
44	20	0.4	1 ADH26701	Human PI3K regulat
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46	20	0.4	1 ADH26741	Human PI3K regulat
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49	20	0.4	1 ADH26754	Human PI3K regulat
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52	20	0.4	1 ADH26797	Human PI3K regulat
53	20	0.4	1 ADH26811	Human PI3K regulat
54	20	0.4	1 ADH26695	Human PI3K regulat
55	20	0.4	1 ADH26735	Human PI3K regulat
56	20	0.4	1 ADH26794	Human PI3K regulat
57	20	0.4	1 ADH26683	Human PI3K regulat
58	20	0.4	1 ADH26704	Human PI3K regulat
59	20	0.4	1 ADH26743	Human PI3K regulat
60	20	0.4	1 ADH26747	Human PI3K regulat
61	20	0.4	1 ADH26750	Human PI3K regulat
62	20	0.4	1 ADH26780	Human PI3K regulat
63	20	0.4	1 ADH26790	Human PI3K regulat
64	20	0.4	1 ADH26805	Human PI3K regulat
65	20	0.4	1 ADH26632	Human PI3K regulat
66	20	0.4	1 ADH26707	Human PI3K regulat
67	20	0.4	1 ADH26723	Human PI3K regulat
68	20	0.4	1 ADH26727	Human PI3K regulat
69	20	0.4	1 ADH26732	Human PI3K regulat
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71	20	0.4	1 ADH26744	Human PI3K regulat
72	20	0.4	1 ADH26768	Human PI3K regulat
73	20	0.4	1 ADH26779	Human PI3K regulat
74	20	0.4	1 ADH26793	Human PI3K regulat
75	20	0.4	1 ADH26798	Human PI3K regulat
76	20	0.4	1 ADH26742	Human PI3K regulat
77	20	0.4	1 ADH26761	Human PI3K regulat
78	20	0.4	1 ADH26692	Human PI3K regulat
79	20	0.4	1 ADH26703	Human PI3K regulat
80	20	0.4	1 ADH26715	Human PI3K regulat
81	20	0.4	1 ADH26716	Human PI3K regulat
82	20	0.4	1 ADH26771	Human PI3K regulat
83	20	0.4	1 ADH26795	Human PI3K regulat
84	20	0.4	1 ADH26690	Human PI3K regulat
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89	20	0.4	1 ADH26807	Human PI3K regulat
90	20	0.4	1 ADH26749	Human PI3K regulat
91	20	0.4	1 ADH26808	Human PI3K regulat
92	20	0.4	1 ADH26793	Human PI3K regulat
93	20	0.4	1 ADH26794	Human PI3K regulat
94	20	0.4	1 ADH26769	Human PI3K regulat
95	20	0.4	1 ADH26784	Human PI3K regulat
96	20	0.4	1 ADH26804	Human PI3K regulat
97	20	0.4	1 ADH26808	Human PI3K regulat
98	20	0.4	1 ADH26713	Human PI3K regulat
99	20	0.4	1 ADH26730	Human PI3K regulat
100	20	0.4	1 ADH26734	Human PI3K regulat
101	20	0.4	1 ADH26791	Human PI3K regulat
102	20	0.4	1 ADH26893	Human PI3K regulat
103	20	0.4	1 ADH26713	Human PI3K regulat
104	20	0.4	1 ADH26724	Human PI3K regulat
105	20	0.4	1 ADH26730	Human PI3K regulat
106	20	0.4	1 ADH26751	Human PI3K regulat

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OM nucleic - nucleic search, using sw model

Run on: August 18, 2005, 08:32:01 ; Search time 9 Seconds

(without alignments)
3.614 Million cell updates/sec

Title: US-10-667-022-4
Perfect score: 5085
Sequence: 1 ggtatccccgggtgcagga.....tcgaggggggccggtaac 5085

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 150 seqs, 3198 residues

Total number of hits satisfying chosen parameters: 300

Minimum DB seq length: 8

Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 150 summaries

Database : fetch4rge.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	1.2	60	1 CQ540998	ACCESSION:CQ540998
2	40.6	0.8	50	1 CQ878333	ACCESSION:CQ878333
C	3	40.6	0.8	50 1 CQ878334	ACCESSION:CQ878334
C	4	33.2	0.7	40 1 AR014711	ACCESSION:AR014711
C	5	33.2	0.7	40 1 I55635	ACCESSION:I55635
C	6	30	0.6	30 1 AR541545	ACCESSION:AR541545
C	7	30	0.6	30 1 AR541546	ACCESSION:AR541546
C	8	27.6	0.5	35 1 AR63566	ACCESSION:AR63566
C	9	27	0.5	35 1 A63565	ACCESSION:A63565
C	10	27	0.5	35 1 A63574	ACCESSION:A63574
C	11	22.6	0.4	30 1 AR559409	ACCESSION:AR559409
C	12	21	0.4	21 1 E13974	ACCESSION:E13974
C	13	21	0.4	21 1 E14908	ACCESSION:E14908
C	14	21	0.4	21 1 E64706	ACCESSION:E64706
C	15	21	0.4	21 1 AR559758	ACCESSION:AR559758
C	16	21	0.4	24 1 A87299	ACCESSION:A87299
C	17	21	0.4	24 1 BD05777	ACCESSION:BD05777
C	18	20	0.4	20 1 AR532682	ACCESSION:AR532682
C	19	20	0.4	1 AR559396	ACCESSION:AR559396
C	20	20	0.4	20 1 AR559111	ACCESSION:AR559111
C	21	20	0.4	20 1 AR561993	ACCESSION:AR561993
C	22	20	0.4	20 1 AR561665	ACCESSION:AR561665
C	23	20	0.4	20 1 AX085176	ACCESSION:AX085176
C	24	20	0.4	20 1 AX085373	ACCESSION:AX085373
C	25	20	0.4	21 1 AR22119	ACCESSION:AR22119
C	26	20	0.4	24 1 CQB55140	ACCESSION:CQB55140
C	27	19.2	0.4	24 1 AXL03668	ACCESSION:AXL03668
C	28	19.2	0.4	24 1 AX546921	ACCESSION:AX546921
C	29	19	0.4	19 1 CQB817044	ACCESSION:CQB817044
C	30	19	0.4	19 1 AR541350	ACCESSION:AR541350
C	31	19	0.4	19 1 AR541351	ACCESSION:AR541351
C	32	19	0.4	19 1 AR541352	ACCESSION:AR541352
C	33	19	0.4	1 AR541353	ACCESSION:AR541353
C	106	0.3			

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OM nucleic - nucleic search, using bw model

Run on: August 18, 2005, 09:13:44 ; Search time 5 seconds

(without alignments)
 3.936 Million cell updates/sec

Title: US-10-667-022-4

Perfect score: 5085
 Sequence: 1 ggatccccgggtcgagga.....tcgaggggggcccgtaacc 5085

Scoring table: IDENTITY NUC
 Gpop 10.0 , Gapext 0.5

Searched: 58 seqs, 1935 residues

Total number of hits satisfying chosen parameters: 116

Minimum DB seq length: 8

Maximum DB seq length: 80

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 58 summaries

Database : fetchfirst.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

Result No.	Score	Query Match Length	DB	ID	Description	RESULT ¹	VERSION	KEYWORDS	SOURCE	ORGANISM	DEFINITION	COMMENT
c 1	44.4	0.9	55	1	CV058129	CV058129	CV058129.1	GI:51521268	EST.	Hordeum vulgare subsp. vulgare	56 bp mRNA linear EST 24-AUG-2004	
c 2	42	0.8	53	1	CV065817	ACCESSION:CV058129	ACCESSION:CV065817		Bordeau vulgare subsp. vulgare			
c 3	41.4	0.8	45	1	CV065098	ACCESSION:CV066098	ACCESSION:CV065817		Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.			
c 4	41.4	0.8	46	1	CV059173	ACCESSION:CV059173	ACCESSION:CV064988	1 (bases 1 to 56)				
c 5	41.4	0.8	48	1	CV064988	ACCESSION:CV05724	ACCESSION:CV05724		Ali,S, Holloway,B. and Taylor,W.C			
c 6	41	0.8	54	1	CV05724	ACCESSION:CV037126	ACCESSION:CV037126		Normalisation of cereal endosperm EST libraries for structural and functional genomic analysis			
c 7	41	0.8	54	1	CV037126	ACCESSION:CV061744	ACCESSION:CV061744		Plant Mol. Biol. Rep. 18, 123-132 (2000)			
c 8	40.4	0.8	46	1	CV061744	ACCESSION:CV063340	ACCESSION:CV063340		Contact: Bill Taylor			
c 9	39.8	0.8	46	1	CV063340	ACCESSION:CV063340	ACCESSION:CV063340		Commonwealth Scientific and Industrial Research Organisation			
c 10	39.6	0.8	51	1	CV059332	ACCESSION:CV062138	ACCESSION:CV062138		Division of Plant Industry, CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia			
c 11	39.4	0.8	43	1	CV062138	ACCESSION:CV062024	ACCESSION:CV062024		Tel: 61 2 6246 5223			
c 12	38.4	0.8	42	1	CV062024	ACCESSION:CV060361	ACCESSION:CV060361		Fax: 61 2 6246 5000			
c 13	36.6	0.7	47	1	CV060361	ACCESSION:CV060559	ACCESSION:CV060559		Email: Bill.Taylor@csiro.au			
c 14	36.6	0.7	47	1	CV060559	ACCESSION:CV060847	ACCESSION:CV060847		Seq primer: M13 reverse primer			
c 15	35.6	0.7	44	1	CV058132	ACCESSION:CV055836	ACCESSION:CV055836		High quality sequence stop: 56.			
c 16	35.6	0.7	47	1	CV058132	ACCESSION:CV061673	ACCESSION:CV061673		Location/Qualifiers			
c 17	35.6	0.7	47	1	CV061673	ACCESSION:CV066153	ACCESSION:CV066153		FEATURES			
c 18	34.8	0.7	43	1	CV066153	ACCESSION:CV064759	ACCESSION:CV064759		SOURCE			
c 19	34.4	0.7	38	1	CV064759	ACCESSION:CV062707	ACCESSION:CV062707		1. .56			
c 20	34.4	0.7	40	1	CV062707	ACCESSION:CV059301	ACCESSION:CV059301		/organism="Hordeum vulgare subsp. vulgare"			
c 21	33.6	0.7	42	1	CV059301	ACCESSION:CV064457	ACCESSION:CV064457		/mol_type="mRNA"			
c 22	33.4	0.7	40	1	CV064457	ACCESSION:CV054826	ACCESSION:CV054826		/cultivar="Himalaya"			
c 23	32.8	0.6	41	1	CV054826	ACCESSION:CV066718	ACCESSION:CV066718		/sub_species="vulgare"			
c 24	32.4	0.6	36	1	CV065718	ACCESSION:CV066327	ACCESSION:CV066327		/db_xref="Taxon:112509"			
c 25	31.4	0.6	35	1	CV065327	ACCESSION:CV0911545	ACCESSION:CV0911545		/clone="BNEL34f4"			
c 26	30.4	0.6	36	1	CV0911545	ACCESSION:CV055204	ACCESSION:CV055204		/tissue_type="endosperm"			
c 27	30.4	0.6	37	1	CV055204	ACCESSION:CV020491	ACCESSION:CV020491		dev_stage="developing endosperm tissue 10, 12, 15 dpa			
c 28	30	0.6	40	1	CV020491	ACCESSION:CV064432	ACCESSION:CV064432		(days post anthesis)"			
c 29	29	0.6	35	1	CV064432	ACCESSION:CV057897	ACCESSION:CV057897		/lab_host="DHBIO (Life Technology)"			
c 30	29.4	0.6	31	1	CV057897	ACCESSION:CP305592	ACCESSION:CP305592		/clone_id="Barley EST endosperm library"			
c 31	27	0.5	28	1	CP305592	ACCESSION:R38731	ACCESSION:R38731		/note="Vector: zipbox; Site_1: Sal I; Site_2: Not I; mRNA was prepared from endosperm tissues of the barley cultivar			
c 32	25	0.5	33	1	R38731	ACCESSION:CV066570	ACCESSION:CV066570					

SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 15

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.